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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=11; day=20; hr=15; min=21; sec=10; ms=32; ]

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Application No: 09492028 Version No: 2.0

**Input Set:****Output Set:**

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| W 402      | Undefined organism found in <213> in SEQ ID (13) |

<110> APPLICANT: Zuker, Charles S.  
The Regents of the University of California

<120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell  
Specific G-Protein Alpha Subunit

<130> FILE REFERENCE: 02307E-092610US

<140> CURRENT APPLICATION NUMBER:09492028

<141> CURRENT FILING DATE:2008-11-20

<150> PRIOR APPLICATION NUMBER: US 60/117,367

<151> PRIOR FILING DATE: 1999-01-27

<160> NUMBER OF SEQ ID NOS: 14

<170> SOFTWARE: PatentIn Ver. 2.1

<210> SEQ ID NO 1

<211> LENGTH: 1503

<212> TYPE: DNA

<213> ORGANISM: Mus sp.

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (157)..(1224)

<223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14  
subunit (TC-Galpha14)

<400> SEQUENCE: 1

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| aactgccttc                                                      | gagaagcggtt | agcctagaga | tccgagcctc | ttctccatac              | catagttggt | 60  |
| tcaggtgggtt                                                     | tcctcttcaa  | accttgcgtc | tgcggataat | ccgcgcggcc              | gggcgttaag | 120 |
| ctccaggtcc                                                      | ctgtcgctcc  | gtcgaggtgg | caagcc     | atg gcc ggc tgc tgc tgt |            | 174 |
|                                                                 |             |            |            | Met Ala Gly Cys Cys Cys |            |     |
|                                                                 |             |            |            | 1                       | 5          |     |
| ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag |             |            |            |                         |            | 222 |
| Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu |             |            |            |                         |            |     |
|                                                                 | 10          | 15         |            | 20                      |            |     |
| cgg cac gtt cgc cgc gac aag aag gac gcg cgc cgg gag ctc aag ctg |             |            |            |                         |            | 270 |
| Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu |             |            |            |                         |            |     |
|                                                                 | 25          | 30         |            | 35                      |            |     |
| ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag |             |            |            |                         |            | 318 |
| Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln |             |            |            |                         |            |     |
|                                                                 | 40          | 45         |            | 50                      |            |     |
| atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc |             |            |            |                         |            | 366 |
| Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly |             |            |            |                         |            |     |
|                                                                 | 55          | 60         |            | 65                      |            | 70  |
| ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg |             |            |            |                         |            | 414 |
| Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met |             |            |            |                         |            |     |
|                                                                 | 75          | 80         |            | 85                      |            |     |
| atc aga gca atg gat acc ctg agg ata caa tac atg tgt gag cag aat |             |            |            |                         |            | 462 |
| Ile Arg Ala Met Asp Thr Leu Arg Ile Gln Tyr Met Cys Glu Gln Asn |             |            |            |                         |            |     |
|                                                                 | 90          | 95         |            | 100                     |            |     |
| aag gaa aat gcc cag atc atc agg gaa gtg gaa gta gac aag gtc act |             |            |            |                         |            | 510 |
| Lys Glu Asn Ala Gln Ile Ile Arg Glu Val Glu Val Asp Lys Val Thr |             |            |            |                         |            |     |
|                                                                 | 105         | 110        |            | 115                     |            |     |
| gca ctc tct aga gac cag gtg gca gcc atc aag cag ctg tgg ctg gat |             |            |            |                         |            | 558 |
| Ala Leu Ser Arg Asp Gln Val Ala Ala Ile Lys Gln Leu Trp Leu Asp |             |            |            |                         |            |     |
|                                                                 | 120         | 125        |            | 130                     |            |     |
| ccc gga atc cag gag tgt tac gac agg agg agg gag tac cag ctg tca |             |            |            |                         |            | 606 |
| Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser |             |            |            |                         |            |     |
|                                                                 | 135         | 140        |            | 145                     |            | 150 |
| gac tct gcc aaa tat tac ctg acg gac att gag cgt atc gcc atg ccc |             |            |            |                         |            | 654 |
| Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile Glu Arg Ile Ala Met Pro |             |            |            |                         |            |     |

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|--------------------------------------------------------------------|-----|--|-----|--|-----|------|
|                                                                    | 155 |  | 160 |  | 165 |      |
| tct ttc gtg cca aca caa cag gat gtg ctt cgt gtt aga gtg ccc acc    |     |  |     |  |     | 702  |
| Ser Phe Val Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr    |     |  |     |  |     |      |
|                                                                    | 170 |  | 175 |  | 180 |      |
| act ggc atc ata gaa tat cca ttc gac ctg gaa aac atc atc ttc cga    |     |  |     |  |     | 750  |
| Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg    |     |  |     |  |     |      |
|                                                                    | 185 |  | 190 |  | 195 |      |
| atg gtg gat gtt ggt ggc cag cga tct gaa cga cgg aaa tgg att cac    |     |  |     |  |     | 798  |
| Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His    |     |  |     |  |     |      |
|                                                                    | 200 |  | 205 |  | 210 |      |
| tgc ttt gag agt gtc acc tcc atc att ttc ttg gtt gct ctg agt gaa    |     |  |     |  |     | 846  |
| Cys Phe Glu Ser Val Thr Ser Ile Ile Phe Leu Val Ala Leu Ser Glu    |     |  |     |  |     |      |
|                                                                    | 215 |  | 220 |  | 225 |      |
| tat gac cag gtt ctg gct gag tgt gac aat gag aac cgc atg gag gag    |     |  |     |  |     | 894  |
| Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn Glu Asn Arg Met Glu Glu    |     |  |     |  |     |      |
|                                                                    | 235 |  | 240 |  | 245 |      |
| agc aaa gcc ctg ttt aga acc atc atc acc tac ccc tgg ttt ctg aac    |     |  |     |  |     | 942  |
| Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Leu Asn    |     |  |     |  |     |      |
|                                                                    | 250 |  | 255 |  | 260 |      |
| tcc tcc gtg att ctg ttc tta aac aag aag gat ctt cta gag gag aaa    |     |  |     |  |     | 990  |
| Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys    |     |  |     |  |     |      |
|                                                                    | 265 |  | 270 |  | 275 |      |
| atc atg tac tct cat cta att agc tac ttc cca gag tac aca gga cca    |     |  |     |  |     | 1038 |
| Ile Met Tyr Ser His Leu Ile Ser Tyr Phe Pro Glu Tyr Thr Gly Pro    |     |  |     |  |     |      |
|                                                                    | 280 |  | 285 |  | 290 |      |
| aag caa gat gtc aaa gcg gcc agg gac ttt atc ctg aag ctg tat caa    |     |  |     |  |     | 1086 |
| Lys Gln Asp Val Lys Ala Ala Arg Asp Phe Ile Leu Lys Leu Tyr Gln    |     |  |     |  |     |      |
|                                                                    | 295 |  | 300 |  | 305 |      |
| gac cag aat cct gac aaa gag aag gtt atc tat tct cac ttc act tgt    |     |  |     |  |     | 1134 |
| Asp Gln Asn Pro Asp Lys Glu Lys Val Ile Tyr Ser His Phe Thr Cys    |     |  |     |  |     |      |
|                                                                    | 315 |  | 320 |  | 325 |      |
| gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac    |     |  |     |  |     | 1182 |
| Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp    |     |  |     |  |     |      |
|                                                                    | 330 |  | 335 |  | 340 |      |
| aca atc cta cag cta aac cta cgg gag ttc aac ttg gtg taa            |     |  |     |  |     | 1224 |
| Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val                |     |  |     |  |     |      |
|                                                                    | 345 |  | 350 |  | 355 |      |
| atggaggggcc tactcctccg agacagaggg tgatctgagc ccttcctgcc tgatctacaa |     |  |     |  |     | 1284 |
| gtgcttctgg accaggacct aaggacatta tgtagcccac aggacagaga tgggtagtgc  |     |  |     |  |     | 1344 |
| aatgtgaaaa atacttcacc aaccctttta agtgtcttta attcttcact gtctaactct  |     |  |     |  |     | 1404 |
| tttctcgcct tttggttgaa cgattaggta tcatttttga gtgggttcccc ctctcctatt |     |  |     |  |     | 1464 |
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<210> SEQ ID NO 2  
<211> LENGTH: 355  
<212> TYPE: PRT  
<213> ORGANISM: Mus sp.  
<220> FEATURE:  
<223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14 subunit (TC-Galpha14)  
<400> SEQUENCE: 2  
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20 25 30  
Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys  
35 40 45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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| Ser | Thr | Phe | Ile | Lys | Gln | Met | Arg | Ile | Ile | His | Gly | Ser | Gly | Tyr | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Glu | Asp | Arg | Lys | Gly | Phe | Thr | Lys | Leu | Val | Tyr | Gln | Asn | Ile | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ala | Met | Gln | Ala | Met | Ile | Arg | Ala | Met | Asp | Thr | Leu | Arg | Ile | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Met | Cys | Glu | Gln | Asn | Lys | Glu | Asn | Ala | Gln | Ile | Ile | Arg | Glu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Val | Asp | Lys | Val | Thr | Ala | Leu | Ser | Arg | Asp | Gln | Val | Ala | Ala | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gln | Leu | Trp | Leu | Asp | Pro | Gly | Ile | Gln | Glu | Cys | Tyr | Asp | Arg | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Glu | Tyr | Gln | Leu | Ser | Asp | Ser | Ala | Lys | Tyr | Tyr | Leu | Thr | Asp | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Arg | Ile | Ala | Met | Pro | Ser | Phe | Val | Pro | Thr | Gln | Gln | Asp | Val | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Val | Arg | Val | Pro | Thr | Thr | Gly | Ile | Ile | Glu | Tyr | Pro | Phe | Asp | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Asn | Ile | Ile | Phe | Arg | Met | Val | Asp | Val | Gly | Gly | Gln | Arg | Ser | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Arg | Lys | Trp | Ile | His | Cys | Phe | Glu | Ser | Val | Thr | Ser | Ile | Ile | Phe |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Val | Ala | Leu | Ser | Glu | Tyr | Asp | Gln | Val | Leu | Ala | Glu | Cys | Asp | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Asn | Arg | Met | Glu | Glu | Ser | Lys | Ala | Leu | Phe | Arg | Thr | Ile | Ile | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Pro | Trp | Phe | Leu | Asn | Ser | Ser | Val | Ile | Leu | Phe | Leu | Asn | Lys | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Leu | Leu | Glu | Glu | Lys | Ile | Met | Tyr | Ser | His | Leu | Ile | Ser | Tyr | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Glu | Tyr | Thr | Gly | Pro | Lys | Gln | Asp | Val | Lys | Ala | Ala | Arg | Asp | Phe |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Leu | Lys | Leu | Tyr | Gln | Asp | Gln | Asn | Pro | Asp | Lys | Glu | Lys | Val | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Ser | His | Phe | Thr | Cys | Ala | Thr | Asp | Thr | Glu | Asn | Ile | Arg | Phe | Val |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Ala | Ala | Val | Lys | Asp | Thr | Ile | Leu | Gln | Leu | Asn | Leu | Arg | Glu | Phe |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Leu | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |
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<210> SEQ ID NO 3

<211> LENGTH: 2771

<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)

<400> SEQUENCE: 3

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<210> SEQ ID NO 4

<211> LENGTH: 2579

<212> TYPE: DNA

<213> ORGANISM: Mus sp.

<220> FEATURE:

<223> OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)

<400> SEQUENCE: 4

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